

rnpbm-19

GenCore version 6.2
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:33:46 ; Search time 520 Seconds
(without alignments)
304.787 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14153951 seqs, 3772896607 residues

Total number of hits satisfying chosen parameters: 28307902

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
- 11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq5:*
- 12: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq6:*
- 13: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 15: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 16: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
- 17: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
- 18: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
- 19: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq6:*
- 20: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:33:46 ; Search time 470 Seconds
(without alignments)
304.787 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggcttttagctat 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14153951 seqs, 3772896607 residues

Total number of hits satisfying chosen parameters: 28307902

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
- 11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq5:*
- 12: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq6:*
- 13: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 15: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 16: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
- 17: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
- 18: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
- 19: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq6:*
- 20: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

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SUMMARIES

GenCore version 6.2
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:33:46 ; Search time 644 Seconds
(without alignments)
304.787 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaattgggaagcccagttacc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 14153951 seqs, 3772896607 residues

Total number of hits satisfying chosen parameters: 28307902

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Published_Applications_NA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
- 9: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
- 10: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq4:*
- 11: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq5:*
- 12: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq6:*
- 13: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
- 15: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
- 16: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
- 17: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
- 18: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq5:*
- 19: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq6:*
- 20: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US60_NEW_PUB.seq:*

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SUMMARIES

GenCore version 6.2
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:23:25 ; Search time 613 Seconds
(without alignments)
420.853 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	21	100.0	2224	6	US-10-027-632-102238	Sequence 102238,

run 16m-20

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:23:25 ; Search time 555 Seconds
(without alignments)
420.853 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggcttttagctat 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
c	1	19	100.0	2224	6	US-10-027-632-102238	Sequence 102238,

rn?bm-30

GenCore version 6.2
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:23:25 ; Search time 759 Seconds
(without alignments)
420.853 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaattgggaagccagttacc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Published_Applications_NA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
- 13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
- 14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
- 15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
- 16: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11D_PUBCOMB.seq:*

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SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	26	100.0	2224	6	US-10-027-632-102238	Sequence 102238,	

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:18:36 ; Search time 66 Seconds
(without alignments)
596.585 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	21	100.0	601	3	US-09-949-016-164991	Sequence 164991,
2	21	100.0	10024	4	US-09-880-107-2430	Sequence 2430, Ap
3	21	100.0	12665	3	US-09-949-016-16388	Sequence 16388, A
4	19.4	92.4	1034	3	US-09-358-856C-7	Sequence 7, Appli
5	19.4	92.4	1034	3	US-09-358-856C-10	Sequence 10, Appl
6	19.4	92.4	1035	3	US-09-358-856C-3	Sequence 3, Appli
7	19.4	92.4	1035	3	US-09-358-856C-5	Sequence 5, Appli

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:18:36 ; Search time 60 Seconds
(without alignments)
596.585 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggcttttagctat 19

Scoring table: IDENTITY_NUC
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Maximum Match 100%
Listing first 200 summaries

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- 1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
 - 2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
 - 8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
 - 9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
 - 10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

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SUMMARIES

		%						Description
Result	Query	Match	Length	DB	ID			
No.	Score							
c 1	19	100.0	601	3	US-09-949-016-164991		Sequence 164991,	
c 2	19	100.0	601	3	US-09-949-016-164992		Sequence 164992,	
c 3	19	100.0	10024	4	US-09-880-107-2430		Sequence 2430, Ap	
c 4	19	100.0	12665	3	US-09-949-016-16388		Sequence 16388, A	
c 5	15.8	83.2	601	3	US-09-949-016-88349		Sequence 88349, A	
c 6	15.8	83.2	601	3	US-09-949-016-88350		Sequence 88350, A	
c 7	15.8	83.2	36016	3	US-09-949-016-14223		Sequence 14223, A	

mi-30

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:18:36 ; Search time 82 Seconds
(without alignments)
596.585 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaattgggaagcccagttacc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : Issued_Patents_NA:*
1: /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	26	100.0	601	3	US-09-949-016-164991	Sequence 164991,
2	26	100.0	601	3	US-09-949-016-164992	Sequence 164992,
3	26	100.0	10024	4	US-09-880-107-2430	Sequence 2430, Ap
4	26	100.0	12665	3	US-09-949-016-16388	Sequence 16388, A
c 5	18.6	71.5	601	3	US-09-949-016-31506	Sequence 31506, A
c 6	18.6	71.5	601	3	US-09-949-016-31507	Sequence 31507, A
7	18.6	71.5	601	3	US-09-949-016-187176	Sequence 187176,

31-19

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:05:50 ; Search time 2126 Seconds
(without alignments)
612.888 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_est13:*
12: gb_est12:*
13: gb_est11:*
14: gb_est10:*
15: gb_gss1:*
16: gb_gss2:*
17: gb_gss3:*
18: gb_gss4:*
19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
 Query

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:05:50 ; Search time 1923 Seconds
(without alignments)
612.888 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggcttttagctat 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_htc:*
7: gb_est2:*
8: gb_est7:*
9: gb_est8:*
10: gb_est9:*
11: gb_est13:*
12: gb_est12:*
13: gb_est11:*
14: gb_est10:*
15: gb_gss1:*
16: gb_gss2:*
17: gb_gss3:*
18: gb_gss4:*
19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
 Query

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:05:50 ; Search time 2632 Seconds
 (without alignments)
 612.888 Million cell updates/sec

Title: US-10-529-447-30
 Perfect score: 26
 Sequence: 1 tggaagctaattgggaagcccagttacc 26

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 53585215 seqs, 31020513797 residues

Total number of hits satisfying chosen parameters: 107170430

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 200 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est3:*
 3: gb_est4:*
 4: gb_est5:*
 5: gb_est6:*
 6: gb_htc:*
 7: gb_est2:*
 8: gb_est7:*
 9: gb_est8:*
 10: gb_est9:*
 11: gb_est13:*
 12: gb_est12:*
 13: gb_est11:*
 14: gb_est10:*
 15: gb_gss1:*
 16: gb_gss2:*
 17: gb_gss3:*
 18: gb_gss4:*
 19: gb_gss5:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
 Result Query

GenCore version 6.2
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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:04:22 ; Search time 1042 Seconds
(without alignments)
1392.959 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_inf:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.		%					
1	21	100.0	21	2	DD309751	DD309751 Method an	
2	21	100.0	134	5	HSPBGD	X68018 H.sapiens g	

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:04:22 ; Search time 943 Seconds
 (without alignments)
 1392.959 Million cell updates/sec

Title: US-10-529-447-20
 Perfect score: 19
 Sequence: 1 cgggacgggcttttagctat 19

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 200 summaries

Database : GenEmbl:*
 1: gb_env:*
 2: gb_pat:*
 3: gb_ph:*
 4: gb_pl:*
 5: gb_pr:*
 6: gb_ro:*
 7: gb_sts:*
 8: gb_sy:*
 9: gb_un:*
 10: gb_vi:*
 11: gb_ov:*
 12: gb_htg:*
 13: gb_in:*
 14: gb_om:*
 15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	19	100.0	19	2	DD309752	DD309752 Method an
c	2	19	100.0	10024	2	AR781867	AR781867 Sequence

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:04:22 ; Search time 1290 Seconds
(without alignments)
1392.959 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaattgggaagcccagttacc 26

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7568541 seqs, 34560148153 residues

Total number of hits satisfying chosen parameters: 15137082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : GenEmbl:*
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_sts:*
8: gb_sy:*
9: gb_un:*
10: gb_vi:*
11: gb_ov:*
12: gb_htg:*
13: gb_in:*
14: gb_om:*
15: gb_ba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	26	100.0	26	2	DD309762	DD309762 Method an
2	26	100.0	10024	2	AR781867	AR781867 Sequence

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:03:24 ; Search time 497 Seconds
(without alignments)
387.865 Million cell updates/sec

Title: US-10-529-447-30
Perfect score: 26
Sequence: 1 tggaagctaattgggaagcccagttacc 26

Scoring table: IDENTITY_NUC.
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	26	100.0	26	12	ADM82975	Adm82975 Human pap

rng-19

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:03:24 ; Search time 401 Seconds
(without alignments)
387.865 Million cell updates/sec

Title: US-10-529-447-19
Perfect score: 21
Sequence: 1 gcctgcagtttgaaatcagtg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	21	100.0	21	12	ADM82967	Adm82967 Human pap	

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OM nucleic - nucleic search, using sw model

Run on: March 31, 2007, 06:03:24 ; Search time 363 Seconds
(without alignments)
387.865 Million cell updates/sec

Title: US-10-529-447-20
Perfect score: 19
Sequence: 1 cgggacgggcttttagctat 19

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5620219 seqs, 3705283702 residues

Total number of hits satisfying chosen parameters: 11240438

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database : N_Geneseq_200701:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*
15: geneseqn2006s:*
16: geneseqn2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
1	19	100.0	19	12	ADM82968		Adm82968 Human pap